

# SEQUENCE LISTING

<110> O'Brien, Timothy J.  
 <120> TADG-15: An Extracellular Serine Protease  
 Overexpressed in Carcinomas  
 <130> D6064CIP  
 <141> 10-20-1999  
 <150> 09/027,337  
 <151> 02-20-1998  
 <160> 98  
 <170> WORD 6.0.1 for Macintosh

<210> 1  
 <211> 3147  
 <212> DNA  
 <213> *Homo sapiens*  
 <220>  
 <223> TADG-15  
 <400> 1

tcaagagcgg	cctcggggta	ccatggggag	cgatcggggc	cgcaagggcg	gagggggccc	60
gaaggacttc	ggcgcgggac	tcaagtacaa	ctcccgccac	gagaaagtga	atggcttgga	120
ggaaggcgtg	gagttcctgc	cagtcaacaa	cgtcaagaag	gtggaaaagc	atggcccggg	180
gcgctgggtg	gtgctggcag	ccgtgctgat	cggtctcttc	ttggtcttgc	tggggatcgg	240
cttcctgggtg	tggcatttgc	agtaccggga	cgtgctgtgc	cagaaggtct	tcaatggcta	300
catgaggatc	acaaatgaga	attttgtgga	tgcctacgag	aactccaact	ccactgagtt	360
tgtaagcctg	gccagcaagg	tgaaggacgc	gctgaagctg	ctgtacagcg	gagtcgccatt	420
cctgggcccc	taccacaagg	agtcggctgt	gacggccttc	agcgagggca	gcgtcatcgc	480
ctactactgg	tctgagttca	gcatcccgcga	gcacctgggtg	gaggaggccg	agcgcgtcat	540
ggccgaggag	cgcgtagtca	tgtctgcccc	gcggggcgcg	tccctgaagt	cctttgtggt	600
cacctcagtg	gtggctttcc	ccacggactc	caaaacagta	cagaggacct	aggacaacag	660
ctgcagcttt	ggcctgcacg	cccgcggtgt	ggagctgatg	cgcttcacca	cgcccggcct	720
ccctgacagc	ccctaccccg	ctcatgcccg	ctgccagtgg	gccttgcggg	gggacgccga	780
ctcagtgtg	agcctcacct	tccgcagctt	tgaccttgcg	tcdtgcgacg	agcgcggcag	840
cgacctgggtg	acggtgtaca	acaccctgag	ccccatggag	ccccacgccc	tggtgcagtt	900
gtgtgggcacc	taccctccct	cctacaacct	gaccttccac	tcctcccaga	acgtcctgct	960
catcacactg	ataaccaaca	ctgagcggcg	gcatcccggc	tttgaggcca	ccttcttcca	1020
gctgcctagg	atgagcagct	gtggaggccg	cttacgtaaa	gcccaggcca	cattcaacag	1080
cccctactac	ccaggccact	acccacccaa	cattgactgc	acatggaaac	ttgaggtgcc	1140
caacaaccag	catgtgaagg	tgagcttcaa	attcttctac	ctgctggagc	ccggcggtgcc	1200
tgcgggcacc	tgccccaagg	actacgtgga	gatcaatggg	gagaaatact	gcggagagag	1260
gtcccagttc	gtcgtcacca	gcaacagcaa	caagatcaca	gttcgcttcc	actcagatca	1320
gtcctacacc	gacaccggct	tcttagctga	atacctctcc	tacgactcca	gtgacccatg	1380
cccggggcag	ttcacgtgcc	gcacggggcg	gtgtatccgg	aaggagctgc	gctgtgatgg	1440
ctggggccgac	tgcaccgacc	acagcgatga	gctcaactgc	agttgcgacg	ccggccacca	1500



Sub  
Al  
w

SEQ-3

000201-ET2160

Val Asn Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys  
 515 520 525  
 Pro Ala Gln Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys  
 530 535 540  
 Ser Gln Gln Cys Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp  
 545 550 555  
 Glu Ala Ser Cys Pro Lys Val Asn Val Val Thr Cys Thr Lys His  
 560 565 570  
 Thr Tyr Arg Cys Leu Asn Gly Leu Cys Leu Ser Lys Gly Asn Pro  
 575 580 585  
 Glu Cys Asp Gly Lys Glu Asp Cys Ser Asp Gly Ser Asp Glu Lys  
 590 595 600  
 Asp Cys Asp Cys Gly Leu Arg Ser Phe Thr Arg Gln Ala Arg Val  
 605 610 615  
 Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val  
 620 625 630  
 Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu  
 635 640 645  
 Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp  
 650 655 660  
 Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe  
 665 670 675  
 Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln  
 680 685 690  
 Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp  
 695 700 705  
 Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro  
 710 715 720  
 Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala  
 725 730 735  
 Ser His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp  
 740 745 750  
 Gly His Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys  
 755 760 765  
 Gly Glu Ile Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu  
 770 775 780  
 Pro Gln Gln Ile Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser  
 785 790 795  
 Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser  
 800 805 810  
 Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly Val Val Ser  
 815 820 825  
 Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val Tyr Thr  
 830 835 840  
 Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly Val  
 845 850 855

<210> 3

<211> 256

<212> PRT

<213> *Homo sapiens*

SEQ-4

<220>

<223> Hepsin

<400> 3

Arg Ile Val Gly Gly Arg Asp Thr Ser Leu Gly Arg Trp Pro Trp  
5 10 15  
Gln Val Ser Leu Arg Tyr Asp Gly Ala His Leu Cys Gly Gly Ser  
20 25 30  
Leu Leu Ser Gly Asp Trp Val Leu Thr Ala Ala His Cys Phe Pro  
35 40 45  
Glu Arg Asn Arg Val Leu Ser Arg Trp Arg Val Phe Ala Gly Ala  
50 55 60  
Val Ala Gln Ala Ser Pro His Gly Leu Gln Leu Gly Val Gln Ala  
65 70 75  
Val Val Tyr His Gly Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser  
80 85 90  
Glu Glu Asn Ser Asn Asp Ile Ala Leu Val His Leu Ser Ser Pro  
95 100 105  
Leu Pro Leu Thr Glu Tyr Ile Gln Pro Val Cys Leu Pro Ala Ala  
110 115 120  
Gly Gln Ala Leu Val Asp Gly Lys Ile Cys Thr Val Thr Gly Trp  
125 130 135  
Gly Asn Thr Gln Tyr Tyr Gly Gln Gln Ala Gly Val Leu Gln Glu  
140 145 150  
Ala Arg Val Pro Ile Ile Ser Asn Asp Val Cys Asn Gly Ala Asp  
155 160 165  
Phe Tyr Gly Asn Gln Ile Lys Pro Lys Met Phe Cys Ala Gly Tyr  
170 175 180  
Pro Glu Gly Gly Ile Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro  
185 190 195  
Phe Val Cys Glu Asp Ser Ile Ser Arg Thr Pro Arg Trp Arg Leu  
200 205 210  
Cys Gly Ile Val Ser Trp Gly Thr Gly Cys Ala Leu Ala Gln Lys  
215 220 225  
Pro Gly Val Tyr Thr Lys Val Ser Asp Phe Arg Glu Trp Ile Phe  
230 235 240  
Gln Ala Ile Lys Thr His Ser Glu Ala Ser Gly Met Val Thr Gln  
245 250 255  
Leu

<210> 4

<211> 225

<212> PRT

<213> *Homo sapiens*

<220>

<223> SCCE

<400> 4

Lys Ile Ile Asp Gly Ala Pro Cys Ala Arg Gly Ser His Pro Trp  
5 10 15

660207-ET2460

mb  
AL  
C/L

Gln	Val	Ala	Leu	Leu	Ser	Gly	Asn	Gln	Leu	His	Cys	Gly	Gly	Val
				20					25					30
Leu	Val	Asn	Glu	Arg	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys	Met
				35					40					45
Asn	Glu	Tyr	Thr	Val	His	Leu	Gly	Ser	Asp	Thr	Leu	Gly	Asp	Arg
				50					55					60
Arg	Ala	Gln	Arg	Ile	Lys	Ala	Ser	Lys	Ser	Phe	Arg	His	Pro	Gly
				65					70					75
Tyr	Ser	Thr	Gln	Thr	His	Val	Asn	Asp	Leu	Met	Leu	Val	Lys	Leu
				80					85					90
Asn	Ser	Gln	Ala	Arg	Leu	Ser	Ser	Met	Val	Lys	Lys	Val	Arg	Leu
				95					100					105
Pro	Ser	Arg	Cys	Glu	Pro	Pro	Gly	Thr	Thr	Cys	Thr	Val	Ser	Gly
				110					115					120
Trp	Gly	Thr	Thr	Thr	Ser	Pro	Asp	Val	Thr	Phe	Pro	Ser	Asp	Leu
				125					130					135
Met	Cys	Val	Asp	Val	Lys	Leu	Ile	Ser	Pro	Gln	Asp	Cys	Thr	Lys
				140					145					150
Val	Tyr	Lys	Asp	Leu	Leu	Glu	Asn	Ser	Met	Leu	Cys	Ala	Gly	Ile
				155					160					165
Pro	Asp	Ser	Lys	Lys	Asn	Ala	Cys	Asn	Gly	Asp	Ser	Gly	Gly	Pro
				170					175					180
Leu	Val	Cys	Arg	Gly	Thr	Leu	Gln	Gly	Leu	Val	Ser	Trp	Gly	Thr
				185					190					195
Phe	Pro	Cys	Gly	Gln	Pro	Asn	Asp	Pro	Gly	Val	Tyr	Thr	Gln	Val
				200					205					210
Cys	Lys	Phe	Thr	Lys	Trp	Ile	Asn	Asp	Thr	Met	Lys	Lys	His	Arg
				215					220					225

<210> 5  
 <211> 225  
 <212> PRT  
 <213> *Homo sapiens*  
 <220>  
 <223> Trypsin  
 <400> 5

Lys	Ile	Val	Gly	Gly	Tyr	Asn	Cys	Glu	Glu	Asn	Ser	Val	Pro	Tyr
				5					10					15
Gln	Val	Ser	Leu	Asn	Ser	Gly	Tyr	His	Phe	Cys	Gly	Gly	Ser	Leu
				20					25					30
Ile	Asn	Glu	Gln	Trp	Val	Val	Ser	Ala	Gly	His	Cys	Tyr	Lys	Ser
				35					40					45
Arg	Ile	Gln	Val	Arg	Leu	Gly	Glu	His	Asn	Ile	Glu	Val	Leu	Glu
				50					55					60
Gly	Asn	Glu	Gln	Phe	Ile	Asn	Ala	Ala	Lys	Ile	Ile	Arg	His	Pro
				65					70					75
Gln	Tyr	Asp	Arg	Lys	Thr	Leu	Asn	Asn	Asp	Ile	Met	Leu	Ile	Lys
				80					85					90
Leu	Ser	Ser	Arg	Ala	Val	Ile	Asn	Ala	Arg	Val	Ser	Thr	Ile	Ser
				95					100					105

660207-CTCT2463

Leu	Pro	Thr	Ala	Pro	Pro	Ala	Thr	Gly	Thr	Lys	Cys	Leu	Ile	Ser
				110					115					120
Gly	Trp	Gly	Asn	Thr	Ala	Ser	Ser	Gly	Ala	Asp	Tyr	Pro	Asp	Glu
				125					130					135
Leu	Gln	Cys	Leu	Asp	Ala	Pro	Val	Leu	Ser	Gln	Ala	Lys	Cys	Glu
				140					145					150
Ala	Ser	Tyr	Pro	Gly	Lys	Ile	Thr	Ser	Asn	Met	Phe	Cys	Val	Gly
				155					160					165
Phe	Leu	Glu	Gly	Gly	Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly
				170					175					180
Pro	Val	Val	Cys	Asn	Gly	Gln	Leu	Gln	Gly	Val	Val	Ser	Trp	Gly
				185					190					195
Asp	Gly	Cys	Ala	Gln	Lys	Asn	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val
				200					205					210
Tyr	Asn	Tyr	Val	Lys	Trp	Ile	Lys	Asn	Thr	Ile	Ala	Ala	Asn	Ser
				215					220					225

<210> 6  
 <211> 231  
 <212> PRT  
 <213> *Homo sapiens*  
 <220>  
 <223> Chymotrypsin  
 <400> 6

Arg	Ile	Val	Asn	Gly	Glu	Asp	Ala	Val	Pro	Gly	Ser	Trp	Pro	Trp
				5					10					15
Gln	Val	Ser	Leu	Gln	Asp	Lys	Thr	Gly	Phe	His	Phe	Cys	Gly	Gly
				20					25					30
Ser	Leu	Ile	Ser	Glu	Asp	Trp	Val	Val	Thr	Ala	Ala	His	Cys	Gly
				35					40					45
Val	Arg	Thr	Ser	Asp	Val	Val	Val	Ala	Gly	Glu	Phe	Asp	Gln	Gly
				50					55					60
Ser	Asp	Glu	Glu	Asn	Ile	Gln	Val	Leu	Lys	Ile	Ala	Lys	Val	Phe
				65					70					75
Lys	Asn	Pro	Lys	Phe	Ser	Ile	Leu	Thr	Val	Asn	Asn	Asp	Ile	Thr
				80					85					90
Leu	Leu	Lys	Leu	Ala	Thr	Pro	Ala	Arg	Phe	Ser	Gln	Thr	Val	Ser
				95					100					105
Ala	Val	Cys	Leu	Pro	Ser	Ala	Asp	Asp	Asp	Phe	Pro	Ala	Gly	Thr
				110					115					120
Leu	Cys	Ala	Thr	Thr	Gly	Trp	Gly	Lys	Thr	Lys	Tyr	Asn	Ala	Asn
				125					130					135
Lys	Thr	Pro	Asp	Lys	Leu	Gln	Gln	Ala	Ala	Leu	Pro	Leu	Leu	Ser
				140					145					150
Asn	Ala	Glu	Cys	Lys	Lys	Ser	Trp	Gly	Arg	Arg	Ile	Thr	Asp	Val
				155					160					165
Met	Ile	Cys	Ala	Gly	Ala	Ser	Gly	Val	Ser	Ser	Cys	Met	Gly	Asp
				170					175					180
Ser	Gly	Gly	Pro	Leu	Val	Cys	Gln	Lys	Asp	Gly	Ala	Trp	Thr	Leu
				185					190					195

Val	Gly	Ile	Val	Ser	Trp	Gly	Ser	Asp	Thr	Cys	Ser	Thr	Ser	Ser
				200					205					210
Pro	Gly	Val	Tyr	Ala	Arg	Val	Thr	Lys	Leu	Ile	Pro	Trp	Val	Gln
				215					220					225
Lys	Ile	Leu	Ala	Ala	Asn									
				230										

<210> 7

<211> 255

<212> PRT

<213> *Homo sapiens*

<220>

<223> Factor 7

<400> 7

Arg	Ile	Val	Gly	Gly	Lys	Val	Cys	Pro	Lys	Gly	Glu	Cys	Pro	Trp
				5					10					15
Gln	Val	Leu	Leu	Leu	Val	Asn	Gly	Ala	Gln	Leu	Cys	Gly	Gly	Thr
				20					25					30
Leu	Ile	Asn	Thr	Ile	Trp	Val	Val	Ser	Ala	Ala	His	Cys	Phe	Asp
				35					40					45
Lys	Ile	Lys	Asn	Trp	Arg	Asn	Leu	Ile	Ala	Val	Leu	Gly	Glu	His
				50					55					60
Asp	Leu	Ser	Glu	His	Asp	Gly	Asp	Glu	Gln	Ser	Arg	Arg	Val	Ala
				65					70					75
Gln	Val	Ile	Ile	Pro	Ser	Thr	Tyr	Val	Pro	Gly	Thr	Thr	Asn	His
				80					85					90
Asp	Ile	Ala	Leu	Leu	Arg	Leu	His	Gln	Pro	Val	Val	Leu	Thr	Asp
				95					100					105
His	Val	Val	Pro	Leu	Cys	Leu	Pro	Glu	Arg	Thr	Phe	Ser	Glu	Arg
				110					115					120
Thr	Leu	Ala	Phe	Val	Arg	Phe	Ser	Leu	Val	Ser	Gly	Trp	Gly	Gln
				125					130					135
Leu	Leu	Asp	Arg	Gly	Ala	Thr	Ala	Leu	Glu	Leu	Met	Val	Leu	Asn
				140					145					150
Val	Pro	Arg	Leu	Met	Thr	Gln	Asp	Cys	Leu	Gln	Gln	Ser	Arg	Lys
				155					160					165
Val	Gly	Asp	Ser	Pro	Asn	Ile	Thr	Glu	Tyr	Met	Phe	Cys	Ala	Gly
				170					175					180
Tyr	Ser	Asp	Gly	Ser	Lys	Asp	Ser	Cys	Lys	Gly	Asp	Ser	Gly	Gly
				185					190					195
Pro	His	Ala	Thr	His	Tyr	Arg	Gly	Thr	Trp	Tyr	Leu	Thr	Gly	Ile
				200					205					210
Val	Ser	Trp	Gly	Gln	Gly	Cys	Ala	Thr	Val	Gly	His	Phe	Gly	Val
				215					220					225
Tyr	Thr	Arg	Val	Ser	Gln	Tyr	Ile	Glu	Trp	Leu	Gln	Lys	Leu	Met
				230					235					240
Arg	Ser	Glu	Pro	Arg	Pro	Gly	Val	Leu	Leu	Arg	Ala	Pro	Phe	Pro
				245					250					255



<210> 8  
 <211> 253  
 <212> PRT  
 <213> *Homo sapiens*  
 <220>  
 <223> Tissue plasminogen activator  
 <400> 8

Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala Ser His Pro Trp  
 5 10 15  
 Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro Gly Glu Arg  
 20 25 30  
 Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser  
 35 40 45  
 Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr  
 50 55 60  
 Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu  
 65 70 75  
 Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp  
 80 85 90  
 Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser  
 95 100 105  
 Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val  
 110 115 120  
 Cys Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys  
 125 130 135  
 Glu Leu Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr  
 140 145 150  
 Ser Glu Arg Leu Lys Glu Ala His Val Arg Leu Tyr Pro Ser Ser  
 155 160 165  
 Arg Cys Thr Ser Gln His Leu Leu Asn Arg Thr Val Thr Asp Asn  
 170 175 180  
 Met Leu Cys Ala Gly Asp Thr Arg Ser Gly Gly Pro Gln Ala Asn  
 185 190 195  
 Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys  
 200 205 210  
 Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile Ser Trp Gly  
 215 220 225  
 Leu Gly Cys Gly Gln Lys Asp Val Pro Gly Val Tyr Thr Lys Val  
 230 235 240  
 Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met Arg Pro  
 245 250

<210> 9  
 <211> 2900  
 <212> DNA  
 <213> *Homo sapiens*  
 <220>

<223> SNC-19; GeneBank Accession No. #U20428

<400> 9

CGCTGGGTGG TGCTGGCAGC CGTGETGATE GGCCTCCTCT TGGTCTTGCT GGGGATCGGC 60  
TTCCTGGTGT GGCATTGCA GTACCGGGAC GTGCGTGTCC AGAAGGTCTT CAATGGCTAC 120  
ATGAGGATCA CAAATGAGAA TTTTGTGGAT GCCTACGAGA ACTCCAATC CACTGAGTTT 180  
GTAAGCCTGG CCAGCAAGGT GAAGGACGCG CTGAAGCTGC TGTACAGCGG AGTCCCATT 240  
CTGGGCCCT ACCACAAGGA GTCGGCTGTG ACGGCCTTCA GCGAGGGCAG CGTCATCGCC 300  
TACTACTGGT CTGAGTTCAG CATCCCGCAG CACCTGGTTG AGGAGGCCGA GCGCGTCATG 360  
GCCAGGAGCG CGTAGTCATG CTGCCCCGCG GGGCGCGCTC CCTGAAGTCC TTTGTGGTCA 420  
CCTCAGGGT GGCTTTCCCC ACGGACTCCA AAACAGTACA GAGGACCCAG GACAACAGCT 480  
GCAGCTTGG CCTGCACGCC GCGGTGTGGA GCTGATGCGC TTCACCACGC CGGCTTCCCT 540  
GACAGCCCT ACCCCGCTCA TGCCCGCTGC CAGTGGGCTG CGGGGACGCG ACGCAGTGCT 600  
GAGCTACTCG AGCTGACTCG CAGCTTGACT GCGCCTCGAC GAGCGCGGCA GCGACCTGGT 660  
GACGTGTACA ACACCTGAG CCCCATGGAG CCCCACGCTT GGTGAGTGTG TGGCACCTAC 720  
CCTCCCTCCT ACAACCTGAC CTTCCACTCC CTCCCACGAA CGTCCTGCTC ATCACACTGA 780  
TAACCAACAC TGACGCGGCA TCCCGGCTTT GAGGCCACCT TCTTCCAGCT GCCTAGGATG 840  
AGCAGCTGTG GAGGCCGCTT ACGTAAAGCC CAGGGGACAT TCAACAGCCC CTACTACCCA 900  
GGCCACTACC CACCAACAT TGACTGCACA TGGAAAATTG AGGTGCCCAA CAACCAGCAT 960  
GTGAAGGTGC GTTCAAATT CTTCTACCTG CTGGAAGCCG GCGTGCTGC GGGCACCTGC 1020  
CCCAAGGACT ACGTGGAGAT CAATGGGGAG AAATACTGCG GAGAGAGGTC CCAGTTCGTC 1080  
GTCACCAGCA ACAGCAACAA GATCACAGTT CGCTTCCACT CAGATCAGTC CTACACCGAC 1140  
ACCGGCTTCT TAGCTGAATA CCTCTCCTAC GACTCCAGTG ACCCATGCC GGGGCAGTTC 1200  
ACGTGCCGCA CGGGGCGGTG TATCCGGAAG GAGCTGCGCT GTGATGGCTG GGCAGCTGCA 1260  
CCGACCACAG CGATGAGCTC AACTGCAGTT GCGACGCCGG CCACCAGTTC ACGTGCAAGA 1320  
GCAAGTTCTG CAAGCTCTTC TGGGTCTGCG ACAGTGTGAA CGAGTGCGGA GACAACAGCG 1380  
ACGAGCAGGG TTGCATTGT CCGGACCCAG ACCTTCAGGT GTTCCAATGG GAAGTGCTC 1440  
TCGAAAAGCC AGCAGTGCAA TGGGAAGGAC GACTGTGGGG ACGGTCGGA CGAGGCCTCC 1500  
TGCCCCAAGG TGAACGTCGT CACTTGTAAC AAACACACCT ACCGCTGCT CAATGGGCTC 1560  
TGCTTGAGCA AGGGCAACCC TGAGTGTGAC GGAAGGAGG ACTGTAGCGA CGGCTCAGAT 1620  
GAGAAGGACT GCGACTGTGG GCTGCGGTCA TTCACGAGAC AGGCTCGTGT TGTGGGGGCG 1680  
ACGGATGCGG ATGAGGGCGA GTGGCCCTGG CAGGTAAGCC TGCATGCTCT GGGCCAGGGC 1740  
CACATCTGCG GTGCTTCCCT CATCTCTCC AACTGGCTGG TCTCTGCCGC ACCTGTCTAC 1800  
ATCGATGACA GAGGATTCAG GTACTCAGAC CCCACGCAGG ACGGCCTTCC TGGGCTTGCA 1860  
CGACCAGAGC CAGCGCAGGC CCTGGGGTGC AGGAGCGCAG GCTCAAGCGC ATCATCTCCC 1920  
ACCCCTTCTT CAATGACTTC ACCTTCGACT ATGACATCGC GCTGCTGGAG CTGGAGAAAC 1980  
CGGCAGAGTA CAGTCCATG GTGCGGCCCA TCTGCCTGCC GGACGCTGC CATGTCTTCC 2040  
CTGCCGGA CAATGACTTC ACCTTCGACT ATGACATCGC GCTGCTGGAG CTGGAGAAAC 1980  
CGCTGATCCT GCAAAAGGGT GAGATCCGCG CGCATGATGT GCGTGGGCTT CCTCAGCGGC GGCCTGGACT 2220  
TGCCGCAGCA GATCACGCCG CGCATGATGT GCGTGGGCTT CCTCAGCGGC GGCCTGGACT 2220  
CCTGCCAGGG TGATTCCGGG GGACCCCTGT CCAGCGTGA GGCAGGATGGG CGGATCTTCC 2280  
AGGCCGGTGT GGTGAGCTGG GGAGACGCTG CGCTCAGAGG AACAAGCCAG GCGTGTACAC 2340  
AAGGTCCTT CTGTTTCGGG AATGGATCAA AGAGAACACT GGGGTATAGG GGCCGGGGCC 2400  
ACCCAAATGT GTACACCTGC GGGGCCACCC ATCGTCCACC CCAGTGTGCA CGCCTGCAGG 2460  
CTGGAGACTC GCGCACCGTG ACCTGCACCA GCGCCCCAGA ACATACACTG TGAATCATC 2520  
TCCAGGCTCA AATCTGCTAG AAAACCTCTC GCTTCTCAG CTTCCAAAGT GGAGCTGGGA 2580  
GGGTAGAAGG GGAGGAACAC TGGTGTTCT ACTGACCCAA CTGGGGCAAG GTTTGAAGCA 2640  
CAGCTCCGGC AGCCCAAGTG GCGGAGGACG CGTTTGTGCA TACTGCCCTG CTCTATACAC 2700  
GGAAGACCTG GATCTCTAGT GAGTGTGACT GCCGGATCTG GCTGTGGTCC TTGGCCACGC 2760  
TTCTTGAGGA AGCCAGGCT CGGAGGACCC TGGAAAACAG ACGGCTCTGA GACTGAAAAT 2820  
GGTTTACCAG CTCCAGGTG ACTTCAGTGT GTGTATTGTG TAAATGAGTA AAACATTTTA 2880  
TTTCTTTTAA AAAAAAAAAA 2900

<210> 10  
 <211> 922  
 <212> PRT  
 <213> *Mus musculus*  
 <220>  
 <223> Epithin  
 <400> 10

Met	Gly	Ser	Asn	Arg	Gly	Arg	Lys	Ala	Gly	Gly	Gly	Ser	Gln	Asp
			5						10					15
Phe	Gly	Ala	Gly	Leu	Lys	Tyr	Asp	Ser	Arg	Leu	Glu	Asn	Met	Asn
			20						25					30
Gly	Phe	Glu	Glu	Gly	Val	Glu	Phe	Leu	Pro	Ala	Asn	Asn	Ala	Lys
			35						40					45
Lys	Val	Glu	Lys	Arg	Gly	Pro	Arg	Arg	Trp	Val	Val	Leu	Val	Ala
			50						55					60
Val	Leu	Phe	Ser	Phe	Leu	Leu	Leu	Ser	Leu	Met	Ala	Gly	Leu	Leu
			65						70					75
Val	Trp	His	Phe	His	Tyr	Arg	Asn	Val	Arg	Val	Gln	Lys	Val	Phe
			80						85					90
Asn	Gly	His	Leu	Arg	Ile	Thr	Asn	Glu	Ile	Phe	Leu	Asp	Ala	Tyr
			95						100					105
Glu	Asn	Ser	Thr	Ser	Thr	Glu	Phe	Ile	Ser	Leu	Ala	Ser	Gln	Val
			110						115					120
Lys	Glu	Ala	Leu	Lys	Leu	Leu	Tyr	Asn	Glu	Val	Pro	Val	Leu	Gly
			125						130					135
Pro	Tyr	His	Lys	Lys	Ser	Ala	Val	Thr	Ala	Phe	Ser	Glu	Gly	Ser
			140						145					150
Val	Ile	Ala	Tyr	Tyr	Trp	Ser	Glu	Phe	Ser	Ile	Pro	Pro	His	Leu
			155						160					165
Ala	Glu	Glu	Val	Asp	Arg	Ala	Met	Ala	Val	Glu	Arg	Val	Val	Thr
			170						175					180
Leu	Pro	Pro	Arg	Ala	Arg	Ala	Leu	Lys	Ser	Phe	Val	Leu	Thr	Ser
			185						190					195
Val	Val	Ala	Phe	Pro	Ile	Asp	Pro	Arg	Met	Leu	Gln	Arg	Thr	Gln
			200						205					210
Asp	Asn	Ser	Cys	Ser	Phe	Ala	Leu	His	Ala	His	Gly	Ala	Ala	Val
			215						220					225
Thr	Arg	Phe	Thr	Thr	Pro	Gly	Phe	Pro	Asn	Ser	Pro	Tyr	Pro	Ala
			230						235					240
His	Ala	Arg	Cys	Gln	Trp	Val	Leu	Arg	Gly	Asp	Ala	Asp	Ser	Val
			245						250					255
Leu	Ser	Leu	Thr	Phe	Arg	Ser	Phe	Asp	Val	Ala	Pro	Cys	Asp	Glu
			260						265					270
His	Gly	Ser	Asp	Leu	Val	Thr	Val	Tyr	Asp	Ser	Leu	Ser	Pro	Met
			275						280					285
Glu	Pro	His	Ala	Val	Val	Arg	Leu	Cys	Gly	Thr	Phe	Ser	Pro	Ser
			290						295					300
Tyr	Asn	Leu	Thr	Phe	Leu	Ser	Ser	Gln	Asn	Val	Phe	Leu	Val	Thr
			305						310					315
Leu	Ile	Thr	Asn	Thr	Gly	Arg	Arg	His	Leu	Gly	Phe	Glu	Ala	Thr

*Sub*  
*cat*

SECRET

Phe	Phe	Gln	Leu	Pro	Lys	Met	Ser	Ser	Cys	Gly	Gly	Val	Leu	Ser	320	325	330
Asp	Thr	Gln	Gly	Thr	Phe	Ser	Ser	Pro	Tyr	Tyr	Pro	Gly	His	Tyr	335	340	345
Pro	Pro	Asn	Ile	Asn	Cys	Thr	Trp	Asn	Ile	Lys	Val	Pro	Asn	Asn	350	355	360
Arg	Asn	Val	Lys	Val	Arg	Phe	Lys	Leu	Phe	Tyr	Leu	Val	Asp	Pro	365	370	375
Asn	Val	Pro	Val	Gly	Ser	Cys	Thr	Lys	Asp	Tyr	Val	Glu	Ile	Asn	380	385	390
Gly	Glu	Lys	Gly	Ser	Gly	Glu	Arg	Ser	Gln	Phe	Val	Val	Ser	Ser	395	400	405
Asn	Ser	Ser	Lys	Ile	Thr	Val	His	Phe	His	Ser	Asp	His	Ser	Tyr	410	415	420
Thr	Asp	Thr	Gly	Phe	Leu	Ala	Glu	Tyr	Leu	Ser	Tyr	Asp	Ser	Asn	425	430	435
Asp	Pro	Cys	Pro	Gly	Met	Phe	Met	Cys	Lys	Thr	Gly	Arg	Cys	Ile	440	445	450
Arg	Lys	Glu	Leu	Arg	Cys	Asp	Gly	Trp	Ala	Asp	Cys	Pro	Asp	Tyr	455	460	465
Ser	Asp	Glu	Arg	Tyr	Cys	Arg	Cys	Asn	Ala	Thr	His	Gln	Phe	Thr	470	475	480
Cys	Lys	Asn	Gln	Phe	Cys	Lys	Pro	Leu	Phe	Trp	Val	Cys	Asp	Ser	485	490	495
Val	Asn	Asp	Cys	Gly	Asp	Gly	Ser	Asp	Glu	Glu	Gly	Cys	Ser	Cys	500	505	510
Pro	Ala	Gly	Ser	Phe	Lys	Cys	Ser	Asn	Gly	Lys	Cys	Leu	Pro	Gln	515	520	525
Ser	Gln	Lys	Cys	Asn	Gly	Lys	Asp	Asn	Cys	Gly	Asp	Gly	Ser	Asp	530	535	540
Glu	Ala	Ser	Cys	Asp	Ser	Val	Asn	Val	Val	Ser	Cys	Thr	Lys	Tyr	545	550	555
Thr	Tyr	Arg	Cys	Gln	Asn	Gly	Leu	Cys	Leu	Ser	Lys	Gly	Asn	Pro	560	565	570
Glu	Cys	Asp	Gly	Lys	Thr	Asp	Cys	Ser	Asp	Gly	Ser	Asp	Glu	Lys	575	580	585
Asn	Cys	Asp	Cys	Gly	Leu	Arg	Ser	Phe	Thr	Lys	Gln	Ala	Arg	Val	590	595	600
Val	Gly	Gly	Thr	Asn	Ala	Asp	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Val	605	610	615
Ser	Leu	His	Ala	Leu	Gly	Gln	Gly	His	Leu	Cys	Gly	Ala	Ser	Leu	620	625	630
Ile	Ser	Pro	Asp	Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Gln	Asp	635	640	645
Asp	Lys	Asn	Phe	Lys	Tyr	Ser	Asp	Tyr	Thr	Met	Trp	Thr	Ala	Phe	650	655	660
Leu	Gly	Leu	Leu	Asp	Gln	Ser	Lys	Arg	Ser	Ala	Ser	Gly	Val	Gln	665	670	675
Glu	Leu	Lys	Leu	Lys	Arg	Ile	Ile	Thr	His	Pro	Ser	Phe	Asn	Asp	680	685	690
Phe	Thr	Phe	Asp	Tyr	Asp	Ile	Ala	Leu	Leu	Glu	Leu	Glu	Lys	Ser	695	700	705
Val	Glu	Tyr	Ser	Thr	Val	Val	Arg	Pro	Ile	Cys	Leu	Pro	Asp	Ala	710	715	720

SEQ-12

	725		730		735
Thr His Val Phe	Pro Ala Gly Lys Ala	Ile Trp Val Thr Gly	Trp		
	740		745		750
Gly His Thr Lys	Glu Gly Gly Thr Gly	Ala Leu Ile Leu Gln	Lys		
	755		760		765
Gly Glu Ile Arg	Val Ile Asn Gln Thr	Thr Cys Glu Asp Leu	Met		
	770		775		780
Pro Gln Gln Ile	Thr Pro Arg Met Met	Cys Val Gly Phe Leu	Ser		
	785		790		795
Gly Gly Val Asp	Ser Cys Gln Gly Asp	Ser Gly Gly Pro Leu	Ser		
	800		805		810
Ser Ala Glu Lys	Asp Gly Arg Met Phe	Gln Ala Gly Val Val	Ser		
	815		820		825
Trp Gly Glu Gly	Cys Ala Gln Arg Asn	Lys Pro Gly Val Tyr	Thr		
	830		835		840
Arg Leu Pro Cys	Ser Ser Gly Leu Asp	Gln Arg Ala His Trp	Gly		
	845		850		855
Ile Ala Ala Trp	Thr Asp Ser Arg Pro	Gln Thr Pro Thr Gly	Met		
	860		865		870
Pro Asp Met His	Thr Trp Ile Gln Glu	Arg Asn Thr Asp Asp	Ile		
	875		900		905
Tyr Ala Val Ala	Ser Pro Pro Gln His	Asn Pro Asp Cys Glu	Leu		
	910		915		920
His Pro					

<210> 11  
 <211> 23  
 <212> DNA  
 <213> Artificial sequence  
 <220>  
 <221> n=Inosine  
 <222> 6, 9, 12, 15, 18  
 <223> Degenerate oligonucleotide primer  
 <400> 11  
 tgggtngtna cngcngcnca ytg

23

<210> 12  
 <211> 20  
 <212> DNA  
 <213> Artificial sequence  
 <220>  
 <221> n=Inosine  
 <222> 3, 6, 9, 12, 18

SEQ-13

000207 ETECHNO

MB  
A  
W

<223> Degenerate oligonucleotide primer

<400> 12

arnggncnc cnswrtncc

20

<210> 13

<211> 12

<212> PRT

<213> *Homo sapiens*

<220>

<223> Fragment of TADG-15

<400> 13

Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly Val

5

10

<210> 14

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> TADG-15 forward oligonucleotide primer

<400> 14

atgacagagg attcaggtac

20

<210> 15

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> TADG-15 reverse oligonucleotide primer

<400> 15

gaaggtgaag tcattgaaga

20

<210> 16

<211> 20

<212> DNA

<213> Artificial sequence

SEQ-14

600207 ETEETHB

hb  
8/1  
w

<220>

<223>  $\beta$ -tubulin forward oligonucleotide primer

<400> 16

cgcatcaacg tgtactacaa

20

<210> 17

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223>  $\beta$ -tubulin reverse oligonucleotide primer

<400> 17

tacgagctgg tggactgaga

20

<210> 18

<211> 3147

<212> RNA

<213> Artificial sequence

<220>

<223> Antisense of TADG-15

<400> 18

uuuuuuuuuu	uuuuuuuuua	aaaagaaaua	aauguuuuuu	cccauuuaca	50
caaaauacaca	cacugaaguc	caccucggga	gcugguaaaa	caauuucagu	100
cucagacccg	ucuguuuucc	aggguccucc	gagccugggc	uuccucaaga	150
gcguggccca	agggcccccac	agcccagauc	cggcagcccc	accaccuua	200
cugaggaggc	uccgaagcuc	cguucccgcu	gcuccuuaca	gacaggggag	250
gcagauauac	acaaacgcgc	cucggcccag	cuuggggcug	gcggggggag	300
cugugucuuc	aaaccuuugc	ccccaguugg	gucaguagaa	ccaccagugu	350
ccuccccuuc	uaccucccag	cuccacuug	gaggcugagg	aagcgagagg	400
uuuucuaggc	agauuuggag	cccuggagau	ugaguucaca	guguauuguu	450
uggggggcgcu	ggugcaguca	gcgguccagu	cuccagccug	caggcgugca	500
cacuggggug	gacgaugggu	ggccccgcag	guguacacau	uuggguggcc	550
ccggcccccua	uaccccagug	uucucuuga	uccagucccg	aaacagaggg	600
agccuugugu	acacgccugg	cuuguuccuc	ugagcgcagc	cgucucccca	650
gcucaccaca	ccggccugga	agauccgccc	auccgcccucc	agcguggaca	700
gggguccccc	ggaaucaccc	uggcaggagu	ccacgccgcc	gcugaggaag	750
cccacgcaca	ucaugcgcgg	cgugaucugc	ugcggcagga	ggucucgca	800
gguggucugg	uugaugacgc	ggaucucacc	cuuuugcagg	aucagcgcgc	850
cagugccucc	auacugggug	ugucccccagc	ccgugaccca	gauggccuug	900
ccggcagggg	agacauggga	ggcguccggc	aggcagaugg	gccgcaaccau	950
ggagcuguac	ucugccgggu	ucuccagcuc	cagcagcgcg	augucauagu	1000
cgaaggugaa	gucauugaag	aagggguggg	agaugaugcg	cuugagccug	1050

Sub  
A  
W

cgccucgca	ccccggggc	gcugcgugg	cucuggucgu	gcaagccag	1100
gaaggccguc	cacugcgugg	ggucugagua	ccugaauccu	cugucaugca	1150
uguagcagug	ugcggcagag	accagccaga	ugggagagau	gagggaagca	1200
ccgcagaugu	ggcccuggcc	cagagcaugc	aggcuuaccu	gccagggccca	1250
cucgcccua	uccgcauccg	ugccccaac	aacacgagcc	ugucucguga	1300
augaccgcag	cccacagucg	caguccuucu	caucugagcc	gucgcuacag	1350
uccuccuucc	cgucacacuc	aggguggcc	uugcucaagc	agagcccauu	1400
gaggcagcgg	uagguguguu	ugguacaagu	gacgacguuc	accuuggggc	1450
aggaggccuc	gucggaccgc	uccccacagu	cguccuuccc	auugcacugc	1500
uggcuuuucg	agaggcacuu	cccauuggaa	caccugaagg	ucuggggcgg	1550
acaacugcac	cccugcucgu	cgcuuguugc	uccgcagucg	uucacacugu	1600
cgcagacca	gaagaggggc	uugcagaacu	uguucuuugca	cgugaacugg	1650
uggccggcg	cgcaacugca	guugagcuca	ucgcuguggu	cggugcaguc	1700
ggcccagcca	ucacagcgca	gcuccuuccg	gauacaccgc	cccugcgggc	1750
acgugaacug	ccccggggcau	gggucacugg	agucguagga	gagguaauca	1800
gcuaagaagc	cggugucggu	guaggacuga	ucugagugga	agcgaacugu	1850
gaucuuguug	cuguuucugg	ugacgacgaa	cugggaccuc	ucuccgcagu	1900
auuucucccc	auugaucucc	acguaguccu	uggggcaggu	gcccgccaggc	1950
acgccgggcu	ccagcaggua	gaagaauuug	aagcucaccu	ucacaugcug	2000
guuguugggc	accucaauuu	uccaugugca	gucaauguug	gguggguagu	2050
ggccugggua	guaggggcug	uugaaugucc	ccugggcuuu	acguaagcgg	2100
ccuccacagc	ugcucauccu	aggcagcugg	aagaaggugg	ccucaaagcc	2150
gggaugccgc	cgucaguguu	ugguuaucag	ugugaugagc	aggacguucu	2200
gggaggagug	gaaggucagg	uuguaggagg	gaggguaggu	gccacacaac	2250
ugcaccaggg	cguggggcuc	cauggggcuc	aggguguugu	acaccgucac	2300
caggucgcug	ccgcgcucgu	cgcaggacgc	aaggucaaa	cugcggaagg	2350
ugaggcucag	cacugagucg	gcguccccc	gcagggccca	cuggcagcgg	2400
gcaugagcgg	gguaagggcu	gucagggaag	ccgggcgugg	ugaagcgcau	2450
cagcuccaca	ccgcggggcu	gcagggcaaa	gcugcagcug	uuguccuggg	2500
uccucuguac	uguuuuggag	uccgugggga	aagccaccac	ugaggugacc	2550
acaaaggacu	ucagggagcg	cgcccgcggg	ggcagcauga	cuacgcgcuc	2600
cucggccaug	acgcgcucgg	ccuccuccac	caggugcugc	gggaugcuga	2650
acucagacca	guaguaggcg	augacgcugc	ccucgcugaa	ggccgucaca	2700
gccgacuccu	ugugguaggg	gcccaggaau	gggacuccgc	uguacagcag	2750
cuucagcgcg	uccuucaccu	ugcuggccag	gcuuacaaac	ucaguggagu	2800
uggaguucuc	guaggcaucc	acaaaauucu	cauuugugau	ccucauguag	2850
ccauugaaga	ccuucuggac	acgcacgucc	cgguacugca	aaugccacac	2900
caggaagccg	aucccagca	agaccaagag	gaggccgauc	agcacggcug	2950
ccagcaccac	ccagcgcccc	gggccaugcu	uuuccaccuu	cuugacguug	3000
uugacuggca	ggaacuccac	gccuuccucc	aagccauuca	cuuucucgug	3050
ccgggaguug	uacuugaguc	ccgcgcgcgaa	guccuucggg	ccccuccgc	3100
ccuugcgggc	ccgaucgcuc	cccaugguac	cccaggcccg	cucuuga	3147

<210> 19

<211> 9

<212> PRT

<213> *Homo sapiens*

 $\langle 220 \rangle$ 

<223> Residues 68-76 of the TADG-15 protein

<400> 19



Val Leu Leu Gly Ile Gly Phe Leu Val

5

<210> 20

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 126-134 of the TADG-15 protein

<400> 20

Leu Leu Tyr Ser Gly Val Pro Phe Leu

5

<210> 21

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 644-652 of the TADG-15 protein

<400> 21

Ser Leu Ile Ser Pro Asn Trp Leu Val

5

<210> 22

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 379-387 of the TADG-15 protein

<400> 22

Lys Val Ser Phe Lys Phe Phe Tyr Leu

5

<210> 23

<211> 9

<212> PRT

SEQ-17

660207 E F F 2460

<213> *Homo sapiens*

<220>

<223> Residues 386-394 of the TADG-15 protein

<400> 23

Tyr Leu Leu Glu Pro Gly Val Pro Ala

5

<210> 24

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 257-265 of the TADG-15 protein

<400> 24

Ser Leu Thr Phe Arg Ser Phe Asp Leu

5

<210> 25

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 762-770 of the TADG-15 protein

<400> 25

Ile Leu Gln Lys Gly Glu Ile Arg Val

5

<210> 26

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 841-849 of the TADG-15 protein

<400> 26

Arg Leu Pro Leu Phe Arg Asp Trp Ile

5

SEQ-18

66027-ET-2400

no  
A1  
in

<210> 27

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 64-72 of the TADG-15 protein

<400> 27

Gly Leu Leu Leu Val Leu Leu Gly Ile

5

<210> 28

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 57-65 of the TADG-15 protein

<400> 28

Val Leu Ala Ala Val Leu Ile Gly Leu

5

<210> 29

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 67-75 of the TADG-15 protein

<400> 29

Leu Val Leu Leu Gly Ile Gly Phe Leu

5

<210> 30

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 379-387 of the TADG-15 protein

<400> 30

Lys Val Ser Phe Lys Phe Phe Tyr Leu

5

<210> 31

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 126-134 of the TADG-15 protein

<400> 31

Leu Leu Tyr Ser Gly Val Pro Phe Leu

5

<210> 32

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 88-96 of the TADG-15 protein

<400> 32

Lys Val Phe Asn Gly Tyr Met Arg Ile

5

<210> 33

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 670-678 of the TADG-15 protein

<400> 33

Thr Gln Trp Thr Ala Phe Leu Gly Leu

5

<210> 34

SEQ-20

660307-ETET2H50

Sub  
A1X  
Cr

<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>  
<223> Residues 119-127 of the TADG-15 protein  
<400> 34  
Lys Val Lys Asp Ala Leu Lys Leu Leu

5

<210> 35  
<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>  
<223> Residues 60-68 of the TADG-15 protein  
<400> 35  
Ala Val Leu Ile Gly Leu Leu Leu Val

5

<210> 36  
<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>  
<223> Residues 62-70 of the TADG-15 protein  
<400> 36  
Leu Ile Gly Leu Leu Val Leu Leu

5

<210> 37  
<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>  
<223> Residues 57-65 of the TADG-15 protein  
<400> 37

Val Leu Ala Ala Val Leu Ile Gly Leu

5

<210> 38

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 61-69 of the TADG-15 protein

<400> 38

Val Leu Ile Gly Leu Leu Leu Val Leu

5

<210> 39

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 146-154 of the TADG-15 protein

<400> 39

Phe Ser Glu Gly Ser Val Ile Ala Tyr

5

<210> 40

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 658-666 of the TADG-15 protein

<400> 40

Tyr Ile Asp Asp Arg Gly Phe Arg Tyr

5

<210> 41

<211> 9

<212> PRT

SEQ-22

660207-ET-2460

So  
H/L  
W

<213> *Homo sapiens*

<220>

<223> Residues 449-457 of the TADG-15 protein

<400> 41

Ser Ser Asp Pro Cys Pro Gly Gln Phe

5

<210> 42

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 401-409 of the TADG-15 protein

<400> 42

Tyr Val Glu Ile Asn Gly Glu Lys Tyr

5

<210> 43

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 387-395 of the TADG-15 protein

<400> 43

Leu Leu Glu Pro Gly Val Pro Ala Gly

5

<210> 44

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 553-561 of the TADG-15 protein

<400> 44

Gly Ser Asp Glu Ala Ser Cys Pro Lys

5

SEQ-23

<210> 45

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 97-105 of the TADG-15 protein

<400> 45

Thr Asn Glu Asn Phe Val Asp Ala Tyr

5

<210> 46

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 110-118 of the TADG-15 protein

<400> 46

Ser Thr Glu Phe Val Ser Leu Ala Ser

5

<210> 47

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 811-819 of the TADG-15 protein

<400> 47

Ser Val Glu Ala Asp Gly Arg Ile Phe

5

<210> 48

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

SEQ-24





<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>  
<223> Residues 153-161 of the TADG-15 protein  
<400> 52  
Ala Tyr Tyr Trp Ser Glu Phe Ser Ile

5

<210> 53  
<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>  
<223> Residues 722-730 of the TADG-15 protein  
<400> 53  
Glu Tyr Ser Ser Met Val Arg Pro Ile

5

<210> 54  
<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>  
<223> Residues 326-334 of the TADG-15 protein  
<400> 54  
Gly Phe Glu Ala Thr Phe Phe Gln Leu

5

<210> 55  
<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>  
<223> Residues 304-312 of the TADG-15 protein  
<400> 55

Thr Phe His Ser Ser Gln Asn Val Leu

5

<210> 56

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 707-715 of the TADG-15 protein

<400> 56

Thr Phe Asp Tyr Asp Ile Ala Leu Leu

5

<210> 57

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 21-29 of the TADG-15 protein

<400> 57

Lys Tyr Asn Ser Arg His Glu Lys Val

5

<210> 58

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 665-673 of the TADG-15 protein

<400> 58

Arg Tyr Ser Asp Pro Thr Gln Trp Thr

5

<210> 59

<211> 9

<212> PRT

SEQ-27

660207 ETT460

sub  
X1  
w1

<213> *Homo sapiens*

<220>

<223> Residues 686-694 of the TADG-15 protein

<400> 59

Ala Pro Gly Val Gln Glu Arg Arg Leu

5

<210> 60

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 12-20 of the TADG-15 protein

<400> 60

Gly Pro Lys Asp Phe Gly Ala Gly Leu

5

<210> 61

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 668-676 of the TADG-15 protein

<400> 61

Asp Pro Thr Gln Trp Thr Ala Phe Leu

5

<210> 62

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 461-469 of the TADG-15 protein

<400> 62

Thr Gly Arg Cys Ile Arg Lys Glu Leu

5

SEQ-28

<210> 63

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 59-67 of the TADG-15 protein

<400> 63

Ala Ala Val Leu Ile Gly Leu Leu Leu

5

<210> 64

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 379-387 of the TADG-15 protein

<400> 64

Lys Val Ser Phe Lys Phe Phe Tyr Leu

5

<210> 65

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 119-127 of the TADG-15 protein

<400> 65

Lys Val Lys Asp Ala Leu Lys Leu Leu

5

<210> 66

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

SEQ-29

<223> Residues 780-788 of the TADG-15 protein

<400> 66

Leu Pro Gln Gln Ile Thr Pro Arg Met

5

<210> 67

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 67-75 of the TADG-15 protein

<400> 67

Leu Val Leu Leu Gly Ile Gly Phe Leu

5

<210> 68

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 283-291 of the TADG-15 protein

<400> 68

Ser Pro Met Glu Pro His Ala Leu Val

5

<210> 69

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 12-20 of the TADG-15 protein

<400> 69

Gly Pro Lys Asp Phe Gly Ala Gly Leu

5

<210> 70

<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>  
<223> Residues 257-265 of the TADG-15 protein  
<400> 70

Ser Leu Thr Phe Arg Ser Phe Asp Leu

5

<210> 71  
<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>  
<223> Residues 180-188 of the TADG-15 protein  
<400> 71

Met Leu Pro Pro Arg Ala Arg Ser Leu

5

<210> 72  
<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>  
<223> Residues 217-225 of the TADG-15 protein  
<400> 72

Gly Leu His Ala Arg Gly Val Glu Leu

5

<210> 73  
<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>  
<223> Residues 173-181 of the TADG-15 protein  
<400> 73

SEQ-31

Met Ala Glu Glu Arg Val Val Met Leu

5

<210> 74

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 267-275 of the TADG-15 protein

<400> 74

Ser Cys Asp Glu Arg Gly Ser Asp Leu

5

<210> 75

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 567-575 of the TADG-15 protein

<400> 75

Cys Thr Lys His Thr Tyr Arg Cys Leu

5

<210> 76

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 724-732 of the TADG-15 protein

<400> 76

Ser Ser Met Val Arg Pro Ile Cys Leu

5

<210> 77

<211> 9

<212> PRT

SEQ-32

660207-ETETED0

Sub  
us  
or



<213> *Homo sapiens*

<220>

<223> Residues 409-417 of the TADG-15 protein

<400> 77

Tyr Cys Gly Glu Arg Ser Gln Phe Val

5

<210> 78

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 495-503 of the TADG-15 protein

<400> 78

Thr Cys Lys Asn Lys Phe Cys Lys Pro

5

<210> 79

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 427-435 of the TADG-15 protein

<400> 79

Val Arg Phe His Ser Asp Gln Ser Tyr

5

<210> 80

<211> 9

<212> PRT

<213> *Homo sapiens*

<220>

<223> Residues 695-703 of the TADG-15 protein

<400> 80

Lys Arg Ile Ile Ser His Pro Phe Phe

5

SEQ-33

<210> 81  
<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>  
<223> Residues 664-672 of the TADG-15 protein  
<400> 81

Phe Arg Tyr Ser Asp Pro Thr Gln Trp

5

<210> 82  
<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>  
<223> Residues 220-228 of the TADG-15 protein  
<400> 82

Ala Arg Gly Val Glu Leu Met Arg Phe

5

<210> 83  
<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>  
<223> Residues 492-500 of the TADG-15 protein  
<400> 83

His Gln Phe Thr Cys Lys Asn Lys Phe

5

<210> 84  
<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>



<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>  
<223> Residues 24-32 of the TADG-15 protein  
<400> 88  
Ser Arg His Glu Lys Val Asn Gly Leu

5

<210> 89  
<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>  
<223> Residues 147-155 of the TADG-15 protein  
<400> 89  
Ser Glu Gly Ser Val Ile Ala Tyr Tyr

5

<210> 90  
<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>  
<223> Residues 715-723 of the TADG-15 protein  
<400> 90  
Leu Glu Leu Glu Lys Pro Ala Glu Tyr

5

<210> 91  
<211> 9  
<212> PRT  
<213> *Homo sapiens*  
<220>  
<223> Residues 105-113 of the TADG-15 protein  
<400> 91



